

#3

0590
1106

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/944,602

DATE: 11/13/2001
 TIME: 13:43:06

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3 <110> APPLICANT: Pecker, Iris
 4 Vlodavsky, Israel
 5 Friedman, Yael
 6 Perets, Tuvia
 8 <120> TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES AND THEIR USE IN
 RESEARCH AND
 9 MEDICAL APPLICATIONS
 11 <130> FILE REFERENCE: 01/22380
 W--> 12 <140> CURRENT APPLICATION NUMBER: US 09/944,602 ✓
 13 <141> CURRENT FILING DATE: 2001-09-04
 15 <150> PRIOR APPLICATION NUMBER: US 09/759,207
 16 <151> PRIOR FILING DATE: 2001-01-16
 18 <150> PRIOR APPLICATION NUMBER: US 09/322,977
 19 <151> PRIOR FILING DATE: 1999-06-01
 21 <150> PRIOR APPLICATION NUMBER: US 09/071,739
 22 <151> PRIOR FILING DATE: 1998-05-01
 24 <150> PRIOR APPLICATION NUMBER: US 08/922,180
 25 <151> PRIOR FILING DATE: 1997-09-02
 27 <160> NUMBER OF SEQ ID NOS: 7
 29 <170> SOFTWARE: PatentIn version 3.1
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 1721
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <400> SEQUENCE: 1
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 41 cgctgggtcc cctctcccct ggcgccctgc cccgacctgc gcaagcacag gacgtcgtgg 180
 43 acctggactt cttcacccag gagcgcgtgc acctggtgag cccctcgctc ctgtccgtca 240
 45 ccattgaagc caacctggcc acggaccgcg ggttcctcat cctcctgggt tctccaaagc 300
 47 ttcgtaacct ggccagaggg ttgtctcctg cgtacctgag gtttggtggc accaagacag 360
 49 acttcctaata ttctgatccc aagaaggaat caacctttga agagagaagt tactggcaat 420
 51 ctcaagtcaa ccaggatatt tgcaaatatg gatccatccc tctgatgtg gaggagaagt 480
 53 tacggttgga atggccctac caggagcaat tgctactccg agaacactac cagaaaaagt 540
 55 tcaagaacag cacctactca agaagctctg tagatgtgct atacactttt gcaaactgct 600
 57 caggactgga cttgatcttt ggcctaaatg cgttattaag aacagcagat ttgcagtgga 660
 59 acagttctaa tgctcagttg ctccctggact actgctcttc caaggggtat aacatttctt 720
 61 gggaactagg caatgaacct aacagtttcc ttaagaaggc tgatattttc atcaatgggt 780
 63 cgcagttagg agaagattat attcaattgc ataaacttct aagaaagtcc accttcaaaa 840
 65 atgcaaaaact ctatggtcct gatgttggtc agcctcgaag aaagacggct aagatgctga 900
 67 agagcttctt gaaggctggg ggagaagtga ttgattcagt tacatggcat cactactatt 960
 69 tgaatggacg gactgctacc aggggaagatt ttctaaacct tgatgtattg gacattttta 1020
 71 tttcatctgt gcaaaaagtt ttccaggtgg ttgagagcac caggcctggc aagaaggtct 1080
 73 ggttagggaga aacaagctct gcatatggag gcggagcgcc cttgctatcc gacacctttg 1140
 75 cagctggcct tatgtggctg gataaaattg gcctgtcagc ccgaatggga atagaagtgg 1200
 77 tgatgaggca agtattcttt ggagcaggaa actaccattt agtggatgaa aacttcgatc 1260
 79 ctttacctga ttattggcta tctcttctgt tcaagaaatt ggtgggcacc aaggtgttaa 1320
 81 tggcaagcgt gcaaggttca aagagaagga agcttcgagt ataccttcat tgcacaaaca 1380

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83 ctgacaatcc aaggtataaa gaaggagatt taactctgta tgccataaac ctccataacg      1440
85 tcaccaagta cttgcgggta ccctatcctt tttctaacaa gcaagtggat aaataccttc      1500
87 taagaccttt gggacctcat ggattacttt ccaaactctgt ccaactcaat ggtctaactc      1560
89 taaagatggg ggatgatcaa accttgccac ctttaatgga aaaacctctc cggccaggaa      1620
91 gttcactggg cttgccagct ttctcatata gtttttttgt gataagaaat gccaaagttg      1680
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97 <211> LENGTH: 543
98 <212> TYPE: PRT
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107 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
108                               20                               25                               30
111 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
112                               35                               40                               45
115 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
116                               50                               55                               60
119 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
120 65                               70                               75                               80
123 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
124                               85                               90                               95
127 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
128                               100                              105                              110
131 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
132                               115                              120                              125
135 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
136                               130                              135                              140
139 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
140 145                              150                              155                              160
143 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
144                               165                              170                              175
147 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
148                               180                              185                              190
151 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
152                               195                              200                              205
155 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
156                               210                              215                              220
159 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
160 225                              230                              235                              240
163 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
164                               245                              250                              255
167 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
168                               260                              265                              270
171 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
172                               275                              280                              285
175 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
176                               290                              295                              300

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179 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
180 305          310          315          320
183 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
184          325          330          335
187 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
188          340          345          350
191 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
192          355          360          365
195 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
196          370          375          380
199 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
200 385          390          395          400
203 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
204          405          410          415
207 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
208          420          425          430
211 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
212          435          440          445
215 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
216          450          455          460
219 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
220 465          470          475          480
223 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
224          485          490          495
227 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
228          500          505          510
231 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
232          515          520          525
235 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
236          530          535          540

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240 <210> SEQ ID NO: 3

241 <211> LENGTH: 1721

242 <212> TYPE: DNA

243 <213> ORGANISM: Homo sapiens

W--> 244 <220> FEATURE:

245 <221> NAME/KEY: CDS

246 <222> LOCATION: (63)..(1691)

247 <223> OTHER INFORMATION:

249 <400> SEQUENCE: 3

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252 ag atg ctg ctg cgc tcg aag cct gcg ctg ccg ccg ccg ctg atg ctg      107
253   Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu
254   1          5          10          15
256 ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga      155
257 Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg
258          20          25          30
260 cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag      203
261 Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu
262          35          40          45

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264	ccg	ctg	cac	ctg	gtg	agc	ccc	tgc	ttc	ctg	tcc	gtc	acc	att	gac	gcc	251
265	Pro	Leu	His	Leu	Val	Ser	Pro	Ser	Phe	Leu	Ser	Val	Thr	Ile	Asp	Ala	
266			50					55					60				
268	aac	ctg	gcc	acg	gac	ccg	cgg	ttc	ctc	atc	ctc	ctg	ggg	tct	cca	aag	299
269	Asn	Leu	Ala	Thr	Asp	Pro	Arg	Phe	Leu	Ile	Leu	Leu	Gly	Ser	Pro	Lys	
270		65					70					75					
272	ctt	cgt	acc	ttg	gcc	aga	ggc	ttg	tct	cct	gcg	tac	ctg	agg	ttt	ggg	347
273	Leu	Arg	Thr	Leu	Ala	Arg	Gly	Leu	Ser	Pro	Ala	Tyr	Leu	Arg	Phe	Gly	
274	80					85					90					95	
276	ggc	acc	aag	aca	gac	ttc	cta	att	ttc	gat	ccc	aag	aag	gaa	tca	acc	395
277	Gly	Thr	Lys	Thr	Asp	Phe	Leu	Ile	Phe	Asp	Pro	Lys	Lys	Glu	Ser	Thr	
278					100					105					110		
280	ttt	gaa	gag	aga	agt	tac	tgg	caa	tct	caa	gtc	aac	cag	gat	att	tgc	443
281	Phe	Glu	Glu	Arg	Ser	Tyr	Trp	Gln	Ser	Gln	Val	Asn	Gln	Asp	Ile	Cys	
282				115					120					125			
284	aaa	tat	gga	tcc	atc	cct	cct	gat	gtg	gag	gag	aag	tta	cgg	ttg	gaa	491
285	Lys	Tyr	Gly	Ser	Ile	Pro	Pro	Asp	Val	Glu	Glu	Lys	Leu	Arg	Leu	Glu	
286			130					135					140				
288	tgg	ccc	tac	cag	gag	caa	ttg	cta	ctc	cga	gaa	cac	tac	cag	aaa	aag	539
289	Trp	Pro	Tyr	Gln	Glu	Gln	Leu	Leu	Arg	Glu	His	Tyr	Gln	Lys	Lys		
290		145					150				155						
292	ttc	aag	aac	agc	acc	tac	tca	aga	agc	tct	gta	gat	gtg	cta	tac	act	587
293	Phe	Lys	Asn	Ser	Thr	Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	
294	160					165					170					175	
296	ttt	gca	aac	tgc	tca	gga	ctg	gac	ttg	atc	ttt	ggc	cta	aat	gcg	tta	635
297	Phe	Ala	Asn	Cys	Ser	Gly	Leu	Asp	Leu	Ile	Phe	Gly	Leu	Asn	Ala	Leu	
298					180					185					190		
300	tta	aga	aca	gca	gat	ttg	cag	tgg	aac	agt	tct	aat	gct	cag	ttg	ctc	683
301	Leu	Arg	Thr	Ala	Asp	Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu	Leu	
302				195					200					205			
304	ctg	gac	tac	tgc	tct	tcc	aag	ggg	tat	aac	att	tct	tgg	gaa	cta	ggc	731
305	Leu	Asp	Tyr	Cys	Ser	Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu	Leu	Gly	
306			210					215					220				
308	aat	gaa	cct	aac	agt	ttc	ctt	aag	aag	gct	gat	att	ttc	atc	aat	ggg	779
309	Asn	Glu	Pro	Asn	Ser	Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	
310		225					230					235					
312	tgc	cag	tta	gga	gaa	gat	tat	att	caa	ttg	cat	aaa	ctt	cta	aga	aag	827
313	Ser	Gln	Leu	Gly	Glu	Asp	Tyr	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	
314	240					245					250					255	
316	tcc	acc	ttc	aaa	aat	gca	aaa	ctc	tat	ggg	cct	gat	gtt	ggg	cag	cct	875
317	Ser	Thr	Phe	Lys	Asn	Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	
318				260					265						270		
320	cga	aga	aag	acg	gct	aag	atg	ctg	aag	agc	ttc	ctg	aag	gct	ggg	gga	923
321	Arg	Arg	Lys	Thr	Ala	Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	
322				275					280					285			
324	gaa	gtg	att	gat	tca	gtt	aca	tgg	cat	cac	tac	tat	ttg	aat	gga	cgg	971
325	Glu	Val	Ile	Asp	Ser	Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	
326			290					295					300				
328	act	gct	acc	agg	gaa	gat	ttt	cta	aac	cct	gat	gta	ttg	gac	att	ttt	1019

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329 Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe
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333 Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro
334 320      325      330      335
336 ggc aag aag gtc tgg tta gga gaa aca agc tct gca tat gga ggc gga      1115
337 Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly
338      340      345      350
340 gcg ccc ttg cta tcc gac acc ttt gca gct ggc ttt atg tgg ctg gat      1163
341 Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp
342      355      360      365
344 aaa ttg ggc ctg tca gcc cga atg gga ata gaa gtg gtg atg agg caa      1211
345 Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln
346      370      375      380
348 gta ttc ttt gga gca gga aac tac cat tta gtg gat gaa aac ttc gat      1259
349 Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp
350      385      390      395
352 cct tta cct gat tat tgg cta tct ctt ctg ttc aag aaa ttg gtg ggc      1307
353 Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly
354 400      405      410      415
356 acc aag gtg tta atg gca agc gtg caa ggt tca aag aga agg aag ctt      1355
357 Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu
358      420      425      430
360 cga gta tac ctt cat tgc aca aac act gac aat cca agg tat aaa gaa      1403
361 Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu
362      435      440      445
364 gga gat tta act ctg tat gcc ata aac ctc cat aac gtc acc aag tac      1451
365 Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr
366      450      455      460
368 ttg cgg tta ccc tat cct ttt tct aac aag caa gtg gat aaa tac ctt      1499
369 Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu
370      465      470      475
372 cta aga cct ttg gga cct cat gga tta ctt tcc aaa tct gtc caa ctc      1547
373 Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu
374 480      485      490      495
376 aat ggt cta act cta aag atg gtg gat gat caa acc ttg cca cct tta      1595
377 Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu
378      500      505      510
380 atg gaa aaa cct ctc cgg cca gga agt tca ctg ggc ttg cca gct ttc      1643
381 Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe
382      515      520      525
384 tca tat agt ttt ttt gtg ata aga aat gcc aaa gtt gct gct tgc atc      1691
385 Ser Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
386      530      535      540
388 tgaaaataaa atatactagt cctgacactg      1721
392 <210> SEQ ID NO: 4
393 <211> LENGTH: 26
394 <212> TYPE: DNA
395 <213> ORGANISM: Artificial sequence

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VERIFICATION SUMMARY

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